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Reviewer: Anne Corrigan

Timestamp: Wed Oct 17 17:45:49 EDT 2007

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Application No: 10534766 Version No: 1.0

Input Set:

Output Set:

Started: 2007-10-02 15:07:00.621

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Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 187 ms

Total Warnings: 1

Total Errors: 0

No. of SeqIDs Defined: 1

Actual SeqID Count: 1

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)

SEQUENCE LISTING

<110> THE SCRIPPS RESEARCH INSTITUTE

BRACEY, Michael H.

HANSON, Michael A.

STEVENS, Raymond C.

CRAVATT, Benjamin F.

<120> CRYSTALLINE FORM OF FATTY ACID AMIDE HYDROLASE (FAAH)

<130> SCRIP1590WO

<140> 10534766

<141> 2007-10-02

<150> PCT/US2003/036125

<151> 2003-11-14

<150> US 60/426,788

<151> 2002-11-14

<160> 1

<170> PatentIn version 3.1

<210> 1

<211> 579

<212> PRT

<213> Rat

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			20					25					30		

Gly	Arg	Gln	Lys	Ala	Arg	Gly	Ala	Ala	Thr	Arg	Ala	Arg	Gln	Lys	Gln
		35					40					45			

Arg	Ala	Ser	Leu	Glu	Thr	Met	Asp	Lys	Ala	Val	Gln	Arg	Phe	Arg	Leu
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Gln	Asn	Pro	Asp	Leu	Asp	Ser	Glu	Ala	Leu	Leu	Thr	Leu	Pro	Leu	Leu
65					70					75				80	

Gln	Leu	Val	Gln	Lys	Leu	Gln	Ser	Gly	Glu	Leu	Ser	Pro	Glu	Ala	Val
			85						90					95	

Phe	Phe	Thr	Tyr	Leu	Gly	Lys	Ala	Trp	Glu	Val	Asn	Lys	Gly	Thr	Asn
			100					105					110		

Cys Val Thr Ser Tyr Leu Thr Asp Cys Glu Thr Gln Leu Ser Gln Ala
115 120 125

Pro Arg Gln Gly Leu Leu Tyr Gly Val Pro Val Ser Leu Lys Glu Cys
130 135 140

Phe Ser Tyr Lys Gly His Asp Ser Thr Leu Gly Leu Ser Leu Asn Glu
145 150 155 160

Gly Met Pro Ser Glu Ser Asp Cys Val Val Val Gln Val Leu Lys Leu
165 170 175

Gln Gly Ala Val Pro Phe Val His Thr Asn Val Pro Gln Ser Met Leu
180 185 190

Ser Phe Asp Cys Ser Asn Pro Leu Phe Gly Gln Thr Met Asn Pro Trp
195 200 205

Lys Ser Ser Lys Ser Pro Gly Gly Ser Ser Gly Gly Glu Gly Ala Leu
210 215 220

Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly
225 230 235 240

Ser Ile Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro
245 250 255

Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly
260 265 270

Gln Thr Ala Val Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu
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Ser Leu Ala Leu Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr
290 295 300

Leu Asp Pro Thr Val Pro Pro Leu Pro Phe Arg Glu Glu Val Tyr Arg
305 310 315 320

Ser Ser Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr
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Met	Pro	Ser	Pro	Ala	Met	Arg	Arg	Ala	Leu	Ile	Glu	Thr	Lys	Gln	Arg	340	345	350	
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Pro	Tyr	Ala	Leu	Glu	Val	Leu	Ser	Ala	Gly	Gly	Leu	Phe	Ser	Asp	Gly	370	375	380	
Gly	Arg	Ser	Phe	Leu	Gln	Asn	Phe	Lys	Gly	Asp	Phe	Val	Asp	Pro	Cys	385	390	395	400
Leu	Gly	Asp	Leu	Ile	Leu	Ile	Leu	Arg	Leu	Pro	Ser	Trp	Phe	Lys	Arg	405	410	415	
Leu	Leu	Ser	Leu	Leu	Leu	Lys	Pro	Leu	Phe	Pro	Arg	Leu	Ala	Ala	Phe	420	425	430	
Leu	Asn	Ser	Met	Arg	Pro	Arg	Ser	Ala	Glu	Lys	Leu	Trp	Lys	Leu	Gln	435	440	445	
His	Glu	Ile	Glu	Met	Tyr	Arg	Gln	Ser	Val	Ile	Ala	Gln	Trp	Lys	Ala	450	455	460	
Met	Asn	Leu	Asp	Val	Leu	Leu	Thr	Pro	Met	Leu	Gly	Pro	Ala	Leu	Asp	465	470	475	480
Leu	Asn	Thr	Pro	Gly	Arg	Ala	Thr	Gly	Ala	Ile	Ser	Tyr	Thr	Val	Leu	485	490	495	
Tyr	Asn	Cys	Leu	Asp	Phe	Pro	Ala	Gly	Val	Val	Pro	Val	Thr	Thr	Val	500	505	510	
Thr	Ala	Glu	Asp	Asp	Ala	Gln	Met	Glu	Leu	Tyr	Lys	Gly	Tyr	Phe	Gly	515	520	525	
Asp	Ile	Trp	Asp	Ile	Ile	Leu	Lys	Lys	Ala	Met	Lys	Asn	Ser	Val	Gly	530	535	540	
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Cys Leu Arg Phe Met Arg Glu Val Glu Gln Leu Met Thr Pro Gln Lys
565 570 575

Gln Pro Ser